

# SEARCH REQUEST FORM

61346

Requestor's Name: Jeanine Goldberg Serial Number: 09/619643  
Date: 2/28/02 Phone: 306-5817 Art Unit: 1634

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Grenbank AI 978199 } translate in 6 frames  
AI 734448

Seq 5 - translate in 6 frames

compare resulting proteins

Point of Contact:  
Barb O'Brien  
Technical Information Specialist  
STIC CM1 6A05 308-4291

## STAFF USE ONLY

Date completed: 2-28-02  
Searcher: 1205  
Terminal time: 20  
Elapsed time: plus 18  
CPU time: \_\_\_\_\_  
Total time: \_\_\_\_\_  
Number of Searches: \_\_\_\_\_  
Number of Databases: \_\_\_\_\_

Search Site  
\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S  
Type of Search  
\_\_\_\_ N.A. Sequence  
618 A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

Vendors  
X IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
GCG Other

***This Page Blank (uspto)***

TOIG of: ai734448 check: 6406 from: 1 to: 582

LOCUS AI734448 582 bp mRNA EST 02-FEB-2000

DEFINITION 606031E07.x1 606 - Ear tissue cDNA library from schmidt lab zea

ACCESSION AI734448

VERSION AI734448.1 GI:5055561

KEYWORDS EST.

SOURCE zea mays.

ORGANISM zea mays.

REFERENCE 1 (bases 1 to 582)

AUTHORS Walbot V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 606031 row: E column: 07.

FEATURES

source

1..582

Location/Qualifiers

/organism="Zea mays"

/cultivar="Ohio43"

/db\_xref="taxon:4577"

/clone\_lib="606 - Ear tissue cDNA library from schmidt lab"

/tissue\_type="mixed"

/dev\_stage="ear length from 0.5 cm - 2.0 cm"

/lab\_host="XLOLR (Stratagene)"

/note="Organ: Immature ear; Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI; Mixed ear tissue cDNA library from Schmidt Lab"

BASE COUNT 158 a 131 c 122 g 170 t 1 others

ORIGIN

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582

TOIG of: ai978199 check: 48 from: 1 to: 442

LOCUS AI978199 442 bp mRNA EST 27-AUG-1999

DEFINITION 614041D10.x2 614 - root cDNA library from Walbot Lab zea mays cDNA.

ACCESSION AI978199

VERSION AI978199.1 GI:5791407

KEYWORDS EST.

SOURCE zea mays.

ORGANISM zea mays.

REFERENCE 1 (bases 1 to 442)

AUTHORS Walbot V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614041 row: D column: 10.

FEATURES

source

1..442

Location/Qualifiers

/organism="Zea mays"

/cultivar="W23"

/db\_xref="taxon:4577"

/clone\_lib="614 - root cDNA library from Walbot Lab"

/tissue\_type="root"

/dev\_stage="3-4 days old"

/lab\_host="XLOLR"

/note="Organ: root; Vector: pBluescriptII SK+; Site\_1: EcoRI; Site\_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

BASE COUNT 126 a 107 c 93 g 116 t

ORIGIN

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442

**This Page Blank (uspto)**

SWQDISXLTGTFILFYICLLGKLIACVHCSRNPPEAGDRALEKPEKVLVSGDGYLHHRMCAWGS  
 80 90 100 110 120 130 140  
 GLEMAVXYTLHEKS  
 PG  
 X

10. SEQ-5\_2 (1-110)  
 AI978199\_2

Initial Score = 10 Optimized Score = 53 Significance = -0.51  
 Residue Identity = 11% Matches = 13 Mismatches = 91  
 Gaps = 0 Conservative Substitutions = 6  
 X 10 20 30 40 50 60 70  
 DNLVHPMKRGSTWALXGRDPRLLDSSWSNELCRLXACQENDKRREKFOXYNTRDLAKKAVINHAFLF  
 TKOVSCPIQOKNNSSMCLPLALFSCVNYTAISRPGNVIPNIKROMFCFSATWTOKXKKVAMLITA  
 X 10 20 30 40 50 60 70  
 YFWVHVAERKQONICFLILGITEFPXGLEMAVXYTLHEKS  
 FLARSLVLTWMTFSLHSLPSWQASHLOSILQEQSRSGSRPRRAOVDPDPOGWTRLSAXTLVCLGQ  
 80 90 100 110 120 130 140  
 SW

11. SEQ-5\_2 (1-110)  
 AI734448\_3

Initial Score = 10 Optimized Score = 42 Significance = -0.51  
 Residue Identity = 9% Matches = 10 Mismatches = 99  
 Gaps = 0 Conservative Substitutions = 1  
 X 10 20  
 DNLVHPMKRGSTWALXGRDPRLL  
 KGAVLSKRTTAPACASVXLHFSHWVYTIQPSQPTGMXFPISKKGCSVASLQHPKMKIKKLHGXSLSW  
 40 50 60 70 80 90 100  
 LLDSSWSNELCRLXACQENDKRREKFOXYNTRDLAKKAVINHAFLFYPFWVHVAERKQONICFLILGITE  
 ODLSCXLTGTFILFYICLLGKLIACVHCSRNPPEAGDRALEKPEKVLVSGDGYLHHRMCAWGRNH  
 110 120 130 140 150 160 170  
 PXGLEMAVXYTLHEKS  
 PXLHRYKGRGHYCRKSS  
 180 190

12. SEQ-5\_2 (1-110)  
 AI734448\_2

Initial Score = 10 Optimized Score = 52 Significance = -0.51  
 Residue Identity = 11% Matches = 13 Mismatches = 91  
 Gaps = 0 Conservative Substitutions = 6  
 X 10 20 30 40  
 DNLVHPMKRGSTWALXGRDPRLLDSSWSNELCRLXACQEG  
 FFFPPFFPFXSKFTSGUTRKAMDHRRTTQKSCPIQOKNNSSMCLPLALFSCVNYTAISRPGNVIP  
 10 20 30 40 50 60 70

50 60 70 80 90 100  
 NDKRREKFOXYNTRDLAKKAVINHAFLFYPFWVHVAERKQONICFLILGITEFPXGLEMAVXYTLHEKS  
 NIKKROMFCFSATWTOKXKKVAMLITAFILARSLVLTWMTFSLHSLPSWQASHLOSILQEQSRSGS  
 80 90 100 110 120 130 140  
 RPYKAGDPRFQGWTRLSAXTLVCLGQASSXSXSROREGSLLPQ  
 150 160 170 180 190

This Page Blank (uspto)



```

Residue Identity ~ 8% Matches ~ 9 Mismatches ~ 92
Gaps ~ 0 Conservative Substitutions ~ 8

TRAPPGTVSMOMITLILNGNGPLGLGKAIPIRFWIAPIPLGAMNFAGYELKKAMIDKESSESTREITL
10 20 30 40 50 60 70
TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKIS
X
60 70 80 90 100
RVLSLEFFSFTIAFLASSXPAKFIAPRGAIQKKPGIAPLKSPGSPFPRMDKI
PRQXSTMQLFYIFGSMLORSNRTSAFYFWELHSRRALRWLYSIHYMKVLEDEGTCCSFAGXDSL
80 90 100 110 120 130 140
VL

4. SEQ-5_6 (1-109)
AI97819_5
Initial Score ~ 16 Optimized Score ~ 47 Significance ~ -0.35
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 88
Gaps ~ 1 Conservative Substitutions ~ 6

HODCPSRHTSVYADDNLVHPMKRGSTWALXGRDPLLLDCCSSWNELCRLXACQEGNDKXKXEFQXVNTDL
10 20 30 40 50 60 70
KIRKXSCWVDHCFLGKISRYVDSLEFFSFTIAFLASSXPAKFIAPRGAIQKKPGIAPLKSPGSPFPRMDKI
X
40 50 60 70 80 90 100
AKKAVINHAFTLEFYFWVHAKEQONICFLIGITPPXGLE-MAVXYTLHEKSGARQRMHLELLPFCWIGQL
80 90 100 110 120 130 140
TCF

5. SEQ-5_6 (1-109)
AI734448_5
Initial Score ~ 16 Optimized Score ~ 47 Significance ~ -0.35
Residue Identity ~ 6% Matches ~ 7 Mismatches ~ 96
Gaps ~ 0 Conservative Substitutions ~ 6

X
10 20 30 40 50 60
TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRYVDSLEFFSFTI
X
70 80 90 100
IIAFLASSXPAKFIAPRGAIQKKPGIAPLKSPGSPFPRMDKI
KAMIKDEKNSSSESTREILPRKQXSTMQLFYIFGSMLORSNRTSAFYFWELHSRRALRWLYSIHYMKVLE
80 90 100 110 120 130 140
DRGTCWSCSFAGXDSLVL
150 160

6. SEQ-5_6 (1-109)
AI734448_4
Initial Score ~ 16 Optimized Score ~ 48 Significance ~ -0.35
Residue Identity ~ 12% Matches ~ 17 Mismatches ~ 87
Gaps ~ 26 Conservative Substitutions ~ 5
X 10 20

```

```

TTCNSDPSLXRDDEXDADCPSPPTSVYADDNLVHPMKRGSPMALXGRDPLLLDCCSSWNELCRLXACQCGN
10 20 30 40 50 60 70
OKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRYVDSLEFFSFTIAFLASSXPAKFIAPRGAIQKKP----
10 20 30 40 50 60 70
DKRXXKFFQXVNTFRDLAKKAVINHAFTLEFYFWVHAKEQONICFLIGITPPXGLEMAVXYTLHEKSGARQ
30 40 50 60 70 80 90 100 110 120 130 140
-----GIAPLKSPGSPFPRMDKI
HMLELLEFCWIGQLPCFVIIRKXSIAPLVKPDVNLKXKKKKKKKK
150 160 170 180 190

7. SEQ-5_6 (1-109)
AI734448_3
Initial Score ~ 14 Optimized Score ~ 41 Significance ~ -0.41
Residue Identity ~ 7% Matches ~ 8 Mismatches ~ 83
Gaps ~ 5 Conservative Substitutions ~ 7

TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRYVDSLEFFSFTIAFLA
X
10 20 30 40 50 60 70
FFFFFFFFFFFRANLHRVXGCRMLWIGXONKGAIVLSK-----RTIAPACASVXLHFHVMVTIO
X
10 20 30 40 50 60
SSXPAKFIAPRGAIQKKPGIAPLKSPGSPFPRMDKI
PSGPGPMGXPIPSIKKGRCSVASIQHPKXNIRKILHGSXLSMODLSCLXLTGIFLYHCLLGIACKVHCS
70 80 90 100 110 120 130
KFSNPEAGDRAIKE
140

8. SEQ-5_6 (1-109)
AI734448_2
Initial Score ~ 14 Optimized Score ~ 46 Significance ~ -0.41
Residue Identity ~ 5% Matches ~ 6 Mismatches ~ 93
Gaps ~ 0 Conservative Substitutions ~ 10

X
10 20 30 40 50 60
TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRYVDSLEFFSFTI
X
70 80 90 100
FLV::SXPAKFIAPRGAIQKKPGIAPLKSPGSPFPRMDKI
NIRKROMPCFCEFAFTWOKXNKKVWMLTIAFLARSVLTLHWNFSLISLPSWAHSLOSSLDEQSRSGGS
80 90 100 110 120 130 140
RPXVAGDPRFQGTRLS
150 160

9. SEQ-5_6 (1-109)
AI97819_3
Initial Score ~ 11 Optimized Score ~ 32 Significance ~ -0.49
Residue Identity ~ 11% Matches ~ 8 Mismatches ~ 59
Gaps ~ 0 Conservative Substitutions ~ 3
TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRYVDSLEFFSFTIAFLA
10 20 30 40 50 60 70

```



```

      80      90      100      X      ONKKAVLSSKRTTAPACASVLFHFSHWYTIOD
      |      |      |      |      |
SSXPAKFTAPRGAIQKKPGIAPLKSPSGSPFPMDKI      X
      |      |      |      |
SOGPTGMXFPISKGRCSVASLHGPRPNKTKKLHGXSLSMODLSCXLTGIFLFIYHCLGLKIACKVHCSK
      40      50      60      70      80      90      100
      |      |      |      |      |
RSNPPEACDRALKPEP
      110      120

```

10. SEQ-5\_6 (1-109)  
AI978199\_2

Initial Score	-	11	Optimized Score	-	42	Significance	-	-0.49
Residue Identity	-	9%	Matches	-	10	Mismatches	-	87
Gaps	-	0	Conservative Substitutions	-			-	6

[illegible]

X  
SFP  
MDKI  
|  
SW  
X

11. SEQ-5-6 (1-109)  
AI978199\_4

Initial Score	=	11	Optimized Score	=	48	Significance	=	-0.49
Residue Identity	=	12%	Matches	=	16	Mismatches	=	81
Gaps	=	15	Conservative Substitutions				=	12

```

X      10      20      30      40      50
TFLMCILYSHLKALRECNQYQKKADVLLLCMDPRKIKKSCMDHCELGKII
|      :      :      :      :      :
APGLPLAHOCLCRXXSCPSLETRVHLGSLRRASPSSGILLLEQXTQAMSLPROXXKMKRIPVSOHERS
10      20      30      40      50      60      70

```

```

60      70      80      90     100
SRVSLFFPSSFIATLASSXPAKFTIAPRGAIKKKGIAP-----LKSSGSPSPRMDKI
      |      |      |      |      |      |      |      |      |
COSSDPCNCFILFLFPGCCREATEHHLPFDIGNYLPVPGXDCIYITFXKXCXTETAIAGANVLLDRTAAH
      80      90     100     110     120     130
LFQ

```

12. SEQ-5\_6 (1-109)  
A1734448\_6

Initial Score	=	11	Optimized Score	=	48	Significance	=	-0.49
Residue Identity	=	12%	Matches	=	16	Mismatches	=	81
Gaps	=	15	Conservative Substitutions	=			=	12

X	10	20	30
TFLMXCILYSHLKALRECN	SQYQK	KADVLL	LLCNDP
	:		:

[illegible]

100 X  
ZKSPSGPSEPRMDKI

TEAHAGAVLLLDRTAPLECYPPMIHSLPCXTRCKFALKKKKKKKKKKK  
150 160 170 180 190

This Page Blank (uspto)

seq-5\_4.res

seq-5\_4.res

seq-5\_4.res

seq-5\_4.res

seq-5\_4.res

seq-5\_4.res

seq-5\_4.res

seq-5\_4.res

4

1  
I  
R  
G

seq-5\_4.res

1  
I  
R  
G

2

seq-5\_4.res

seq-5\_4.res

4

1 I  
2 I  
3 R  
4 G

1 I  
2 R  
3 G

seq-5\_4.res

4

1 I  
2 I R  
3 G

seq-5\_4.res

4

1  
I  
I  
R  
R  
G

2  
I  
P  
G

seq-5\_4.res

4

1  
I  
R  
G

2  
1  
R  
G

seq-5\_4.res

4

s  
I  
I  
R  
G

1  
1  
1  
R  
G

2  
I  
R  
G

seq-5\_4.res

4

1  
I  
R  
G

2  
I  
R  
G

seq-5\_4.res

4

1  
I  
R  
G

2  
I  
R  
G

3

seq-5\_4.res

4

1 I  
2 I  
3 I  
4 I  
5 I  
6 I  
7 I  
8 I  
9 I  
10 I  
11 I  
12 I  
13 I  
14 I  
15 I  
16 I  
17 I  
18 I  
19 I  
20 I  
21 I  
22 I  
23 I  
24 I  
25 I  
26 I  
27 I  
28 I  
29 I  
30 I  
31 I  
32 I  
33 I  
34 I  
35 I  
36 I  
37 I  
38 I  
39 I  
40 I  
41 I  
42 I  
43 I  
44 I  
45 I  
46 I  
47 I  
48 I  
49 I  
50 I  
51 I  
52 I  
53 I  
54 I  
55 I  
56 I  
57 I  
58 I  
59 I  
60 I  
61 I  
62 I  
63 I  
64 I  
65 I  
66 I  
67 I  
68 I  
69 I  
70 I  
71 I  
72 I  
73 I  
74 I  
75 I  
76 I  
77 I  
78 I  
79 I  
80 I  
81 I  
82 I  
83 I  
84 I  
85 I  
86 I  
87 I  
88 I  
89 I  
90 I  
91 I  
92 I  
93 I  
94 I  
95 I  
96 I  
97 I  
98 I  
99 I  
100 I  
101 I  
102 I  
103 I  
104 I  
105 I  
106 I  
107 I  
108 I  
109 I  
110 I  
111 I  
112 I  
113 I  
114 I  
115 I  
116 I  
117 I  
118 I  
119 I  
120 I  
121 I  
122 I  
123 I  
124 I  
125 I  
126 I  
127 I  
128 I  
129 I  
130 I  
131 I  
132 I  
133 I  
134 I  
135 I  
136 I  
137 I  
138 I  
139 I  
140 I  
141 I  
142 I  
143 I  
144 I  
145 I  
146 I  
147 I  
148 I  
149 I  
150 I  
151 I  
152 I  
153 I  
154 I  
155 I  
156 I  
157 I  
158 I  
159 I  
160 I  
161 I  
162 I  
163 I  
164 I  
165 I  
166 I  
167 I  
168 I  
169 I  
170 I  
171 I  
172 I  
173 I  
174 I  
175 I  
176 I  
177 I  
178 I  
179 I  
180 I  
181 I  
182 I  
183 I  
184 I  
185 I  
186 I  
187 I  
188 I  
189 I  
190 I  
191 I  
192 I  
193 I  
194 I  
195 I  
196 I  
197 I  
198 I  
199 I  
200 I  
201 I  
202 I  
203 I  
204 I  
205 I  
206 I  
207 I  
208 I  
209 I  
210 I  
211 I  
212 I  
213 I  
214 I  
215 I  
216 I  
217 I  
218 I  
219 I  
220 I  
221 I  
222 I  
223 I  
224 I  
225 I  
226 I  
227 I  
228 I  
229 I  
230 I  
231 I  
232 I  
233 I  
234 I  
235 I  
236 I  
237 I  
238 I  
239 I  
240 I  
241 I  
242 I  
243 I  
244 I  
245 I  
246 I  
247 I  
248 I  
249 I  
250 I  
251 I  
252 I  
253 I  
254 I  
255 I  
256 I  
257 I  
258 I  
259 I  
260 I  
261 I  
262 I  
263 I  
264 I  
265 I  
266 I  
267 I  
268 I  
269 I  
270 I  
271 I  
272 I  
273 I  
274 I  
275 I  
276 I  
277 I  
278 I  
279 I  
280 I  
281 I  
282 I  
283 I  
284 I  
285 I  
286 I  
287 I  
288 I  
289 I  
290 I  
291 I  
292 I  
293 I  
294 I  
295 I  
296 I  
297 I  
298 I  
299 I  
300 I  
301 I  
302 I  
303 I  
304 I  
305 I  
306 I  
307 I  
308 I  
309 I  
310 I  
311 I  
312 I  
313 I  
314 I  
315 I  
316 I  
317 I  
318 I  
319 I  
320 I  
321 I  
322 I  
323 I  
324 I  
325 I  
326 I  
327 I  
328 I  
329 I  
330 I  
331 I  
332 I  
333 I  
334 I  
335 I  
336 I  
337 I  
338 I  
339 I  
340 I  
341 I  
342 I  
343 I  
344 I  
345 I  
346 I  
347 I  
348 I  
349 I  
350 I  
351 I  
352 I  
353 I  
354 I  
355 I  
356 I  
357 I  
358 I  
359 I  
360 I  
361 I  
362 I  
363 I  
364 I  
365 I  
366 I  
367 I  
368 I  
369 I  
370 I  
371 I  
372 I  
373 I  
374 I  
375 I  
376 I  
377 I  
378 I  
379 I  
380 I  
381 I  
382 I  
383 I  
384 I  
385 I  
386 I  
387 I  
388 I  
389 I  
390 I  
391 I  
392 I  
393 I  
394 I  
395 I  
396 I  
397 I  
398 I  
399 I  
400 I  
401 I  
402 I  
403 I  
404 I  
405 I  
406 I  
407 I  
408 I  
409 I  
410 I  
411 I  
412 I  
413 I  
414 I  
415 I  
416 I  
417 I  
418 I  
419 I  
420 I  
421 I  
422 I  
423 I  
424 I  
425 I  
426 I  
427 I  
428 I  
429 I  
430 I  
431 I  
432 I  
433 I  
434 I  
435 I  
436 I  
437 I  
438 I  
439 I  
440 I  
441 I  
442 I  
443 I  
444 I  
445 I  
446 I  
447 I  
448 I  
449 I  
450 I  
451 I  
452 I  
453 I  
454 I  
455 I  
456 I  
457 I  
458 I  
459 I  
460 I  
461 I  
462 I  
463 I  
464 I  
465 I  
466 I  
467 I  
468 I  
469 I  
470 I  
471 I  
472 I  
473 I  
474 I  
475 I  
476 I  
477 I  
478 I  
479 I  
480 I  
481 I  
482 I  
483 I  
484 I  
485 I  
486 I  
487 I  
488 I  
489 I  
490 I  
491 I  
492 I  
493 I  
494 I  
495 I  
496 I  
497 I  
498 I  
499 I  
500 I  
501 I  
502 I  
503 I  
504 I  
505 I  
506 I  
507 I  
508 I  
509 I  
510 I  
511 I  
512 I  
513 I  
514 I  
515 I  
516 I  
517 I  
518 I  
519 I  
520 I  
521 I  
522 I  
523 I  
524 I  
525 I  
526 I  
527 I  
528 I  
529 I  
530 I  
531 I  
532 I  
533 I  
534 I  
535 I  
536 I  
537 I  
538 I  
539 I  
540 I  
541 I  
542 I  
543 I  
544 I  
545 I  
546 I  
547 I  
548 I  
549 I  
550 I  
551 I  
552 I  
553 I  
554 I  
555 I  
556 I  
557 I  
558 I  
559 I  
560 I  
561 I  
562 I  
563 I  
564 I  
565 I  
566 I  
567 I  
568 I  
569 I  
570 I  
571 I  
572 I  
573 I  
574 I  
575 I  
576 I  
577 I  
578 I  
579 I  
580 I  
581 I  
582 I  
583 I  
584 I  
585 I  
586 I  
587 I  
588 I  
589 I  
590 I  
591 I  
592 I  
593 I  
594 I  
595 I  
596 I  
597 I  
598 I  
599 I  
600 I  
601 I  
602 I  
603 I  
604 I  
605 I  
606 I  
607 I  
608 I  
609 I  
610 I  
611 I  
612 I  
613 I  
614 I  
615 I  
616 I  
617 I  
618 I  
619 I  
620 I  
621 I  
622 I  
623 I  
624 I  
625 I  
626 I  
627 I  
628 I  
629 I  
630 I  
631 I  
632 I  
633 I  
634 I  
635 I  
636 I  
637 I  
638 I  
639 I  
640 I  
641 I  
642 I  
643 I  
644 I  
645 I  
646 I  
647 I  
648 I  
649 I  
650 I  
651 I  
652 I  
653 I  
654 I  
655 I  
656 I  
657 I  
658 I  
659 I  
660 I  
661 I  
662 I  
663 I  
664 I  
665 I  
666 I  
667 I  
668 I  
669 I  
670 I  
671 I  
672 I  
673 I  
674 I  
675 I  
676 I  
677 I  
678 I  
679 I  
680 I  
681 I  
682 I  
683 I  
684 I  
685 I  
686 I  
687 I  
688 I  
689 I  
690 I  
691 I  
692 I  
693 I  
694 I  
695 I  
696 I  
697 I  
698

seq-5\_4.res

seq-5\_4.res

1

T  
R  
G

seq-5\_4.res

seq-5\_4.res

4

1  
I  
R  
G

2  
I  
R  
G

seq-5\_4.res

4

1  
I  
R  
G

2  
I  
R  
G

seq-5\_4.res

4

1  
1  
R  
G

2  
1  
R  
G

seq-5\_4.res

4

1 I  
2 I R  
3 I R G  
4 I

Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 93  
Gaps ~ 9 Conservative Substitutions ~ 5

X  
ALFSCNYYTTAISRPYGNVPIPIKRRQMFCCFSATWTOKXNKVAMLTAFIARSLVLTTHNFS-----  
NKTSELSPAKEDQLOLVPLSSSTFLMKCILYSHLKALRECNQYOKKADVLLLCNMDPKIKKXSCVNDH  
X 10 20 30 40 50 60 70

-HLISLPSMOAHSLOSSLQEOSSRRSGSRPRXRAQVDPFRQGWTRL  
CFLGKISRVDSLEFFSSFLIAFPAKFIAPRGAIQOKKGIAPLASPSGSPFRMDKIITCIGTGVPGG  
80 90 100 110 120 130 140

AVLV

#### 4. SEQ-5\_4 (1-111) A1978199\_6

Initial Score ~ 13 Optimized Score ~ 48 Significance ~ -0.39  
Residue Identity ~ 9% Matches ~ 11 Mismatches ~ 97  
Gaps ~ 0 Conservative Substitutions ~ 3

X  
ALFSCNYYTTAISRPYGNVPIPIKRRQMFCCFSATWTOK  
TRTAPPGTSPVSMOMIILICNEGLGFKGAIPIRFWIAPLGAMNFAGYELAKKAMIKDKNSESETRLL  
10 20 30 40 50 60 70

X  
KXNKVAMLTAFIARSLVLTTHNFSHLISLPSMOAHSLOSSLQEOSSRRSGSRPRXRAQVDPFRQGWTRL  
PRKXSTWQLEFFLEFSGMLQSRNMTSAFFXYWELSRRLRWLYSIHYMKRVLEDRGTCWSCCSFAGXDSSL  
80 90 100 110 120 130 140

X  
S  
VL  
X

#### 5. SEQ-5\_4 (1-111) A1734448\_5

Initial Score ~ 13 Optimized Score ~ 48 Significance ~ -0.39  
Residue Identity ~ 9% Matches ~ 11 Mismatches ~ 97  
Gaps ~ 0 Conservative Substitutions ~ 3

GLAAIVTPPEDVKKXHMMPAPGPSPVSMOMIILICNEGLGFKGAIPIRFWIAPLGAMNFAGYELAKKA  
10 20 30 40 50 60 70

IKKRMFCCFSATWTOKXNKVAMLTAFIARSLVLTTHNFSHLISLPSMOAHSLOSSLQEOSSRRSGSR  
MFKDENSSSESTREILPRKXSTWQLEFFLEFSGMLQSRNMTSAFFXYWELSRRLRWLYSIHYMKRVLEDR  
80 90 100 110 120 130 140

PXRAQVDPFRQGWTRL

GTWCSCCSFAGXDSSLVLLSADDPXPSTLNPXICSKKKKKKKKKKK  
150 160 170 180 190

6. SEQ-5\_4 (1-111)  
A1734448\_1 TOIG of: a1734448 check: 6406 from: 1 to: 582

Initial Score ~ 13 Optimized Score ~ 53 Significance ~ -0.39  
Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 88  
Gaps ~ 0 Conservative Substitutions ~ 11

FFFFFEFFFEQIYIGFKKEGYSADNKTRELSYPAKEQOLOHVPLSSSTFLMKCILYSHLKALRECNQ  
10 20 30 40 50 60 70  
X  
ALFSCNYYTTAISRPYGNVPI  
IKKRMFCCFSATWTOKXNKVAMLTAFIARSLVLTTHNFSHLISLPSMOAHSLOSSLQEOSSRRSGSR  
10 20 30 40 50 60 70 80 90  
YOKXADVLLLCNMDPKIKKXSCVNDHCFLEKISRVDSLEFFSSFLIAFPAKFIAPRGAIQOKKGI  
80 90 100 110 120 130 140

PXRAQVDPFRQGWTRL  
PLKSPRGSPFRMDKIITCIGTGVPGGAGIIXFTTSKGVTTIASPPD  
130 160 170 180 190

#### 7. SEQ-5\_4 (1-111) A1978199\_4

Initial Score ~ 12 Optimized Score ~ 44 Significance ~ -0.42  
Residue Identity ~ 4% Matches ~ 5 Mismatches ~ 96  
Gaps ~ 0 Conservative Substitutions ~ 5

X  
ALFSCNYYTTAISRPYGNVPIPIKRRQMFCCFSATWTOKXNKVAMLTAFIARSLVLTTHNFSHLISLPSW  
AGELPQAHQCCLCRXSCPSLETRVHLGSLRARSPASSGLLLEQXTLOAMSLPRKXKMKRIPVS  
X 10 20 30 40 50 60 70

QAHSLQSSLQEOSSRRSGSRPRXRAQVDPFRQGWTRL

QHEASCOESSDQPCNFITLFLGPGCCREATEHLPPFDIGNVPIPGXDGCIVYITXKRCXRTAHAGAVLL  
70 80 90 100 110 120 130

DKTAHLFC  
140

#### 8. SEQ-5\_4 (1-111) A1734448\_4

Initial Score ~ 12 Optimized Score ~ 39 Significance ~ -0.42  
Residue Identity ~ 11% Matches ~ 10 Mismatches ~ 73  
Gaps ~ 0 Conservative Substitutions ~ 6

ALFSCNYYTTAISRPYGNVPIPIKRRQMFCCFSATWTOKXNKVAMLTAFIARSLVLTTHNFSHLISLPSW  
VMRTCGNSDPSLXDEHDDACPSRPTSVYADDNLVHPMKRGSPWALXGR  
10 20 30 40 50 60 70 80 90 100 110 120

QAHSLQSSLQEOSSRRSGSRPRXRAQVDPFRQGWTRL  
DPELLDGSWSNELCRIXACQSGNKRKREKFOXVVTROLAKKAVJNHATFLFFYVNVHAEQONICFLIL  
60 70 80 90 100 110 120

G11PXYGLEMAVYVTLH  
130

#### 9. SEQ-5\_4 (1-111) A1734448\_6

Initial Score = 11 Optimized Score = 46 Significance = -0.44  
Residue Identity = 9% Matches = 11 Mismatches = 93  
Gaps = 0 Conservative Substitutions = 7

X 10 20 30 40 50 60 70  
ALFSCNYYTAISRPYGNVPIPNIKKROMFCCFSATWTOKXNKVAMLTALARSVLVTHNFSHLSPS  
LEDLRQXXPLPLTXXHGXCLPLAHQGLCRXXSCPSLETVPGLSLRARSPPASSGLLLEQXTLOAMSIPR  
X 10 20 30 40 50 60 70

WOAHSLQSSLLQEOSSRRSGSRPRAYDPRFGWTRLS  
FOXXMRRIPIVSOHERSCQESSDPCNFIFLFGPCREATEHLPFDIGNIPIVGPXDGIYITXEXCMR  
80 90 100 110 X 120 130 140

TEAHGAVVLLDRTAPL  
150 160

10. SEO-5\_4 (1-111)  
AI978199\_5

Initial Score = 10 Optimized Score = 52 Significance = -0.47  
Residue Identity = 13% Matches = 15 Mismatches = 90  
Gaps = 0 Conservative Substitutions = 6

X 10 20 30  
ALFSCNYYTAISRPYGNVPIPNIKKROMFCCFSATWT  
HODCPRIITSYADDNLVHPWKRGSSTWALXGRDPLLDCCSSWSNELCRLXACQEGNDKRXEKFQXVNTDRL  
10 20 30 X 40 50 60 70

40 50 60 70 80 90 100  
OKXNKVAMLTALARSVLVTHNFSHLSPSWOAHSLQSSLLQEOSSRRSGSRPRAYDPRFGWTR  
AKKAVINATLETFYFWVAEKOONICLFILGITFPXGLEMAVYITLHEKRSARQRMLELLFFCWIGOLT  
80 90 100 110 120 130 140

110  
LS  
CF  
X

11. SEO-5\_4 (1-111)  
AI978199\_3

Initial Score = 8 Optimized Score = 50 Significance = -0.52  
Residue Identity = 15% Matches = 18 Mismatches = 86  
Gaps = 7 Conservative Substitutions = 7

X 10 20 30 40 50  
ALFSCNYYTAISRPYGNVPIPNIKKROMFCCFSATWTOKXNKVAMLTALARSVLV  
ONKXAVLSKRTTAPACASVLIHFSHVMTIOPSQPTGMXPRIISKGCSVASLOHGPKNKIKKLHGXSLL  
10 20 30 40 50 60 70

60 70 80 90 100 110  
LTHNFSHLSPSWOAHSLQSSLLQEOSSRRSGSRPRAYDPRFGWTRLS  
SMODLSCLTGTGIFLIFYHCLLKLACKVHCSCRSPNEPAGDRALKEPKGTLVSKDGODYHLHRHCAWGRS  
80 90 100 110 120 X 130 140

PG

12. SEO-5\_4 (1-111)  
AI734448\_3

Initial Score = 8 Optimized Score = 18 Significance = -0.52

Residue Identity = 1% Matches = 1 Mismatches = 45  
Gaps = 0 Conservative Substitutions = 5

X 10 20  
ALFSCNYYTAISRPYGNVPIPN  
IKRLGXSLLSMODLSCLTGTGIFLIFYHCLLKLACKVHCSCRSPNEPAGDRALKEPKGTLVSKDGODYHL  
100 110 120 130 140 X 150 160

IKKROMFCCFSATWTOKXNKVAMLTALARSVLVTHNFSHLSPSWOAHSLQSSLLQEOSSRRSGSR  
HRHMAWNRGRHHPXLHNVKRGHGYCRKSS  
170 180 190 X

100  
PYRAOVD

This Page Blank (USP10)

> 0 <  
0110 Intelligenetics  
> 0 <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file seq-5\_2.res made by bobryen on Thu 28 Feb 102 15:45:27 -PST.

Query sequence being compared: SEQ-5\_2 (1-110)  
Number of sequences searched: 12  
Number of scores above cutoff: 12

Results of the initial comparison of SEQ-5\_2 (1-110) with:  
File: genbanktrans.pep

Seq 5, translation frame 2

100-  
N -  
U -50-  
M -  
B -  
E -  
R -  
O -  
F -10-  
S -  
E -5-  
Q -  
U -  
V -  
E -  
C -  
N -  
S -  
SCORE 0 12 24 36 48 61 73 85 97 109  
STDDEV 0 1 1 1 1 1 1 1 1 1 2

PARAMETERS

Similarity matrix PAM-150 K-tuple 1  
Threshold level of sim. 16%  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 5.00 Window size 110  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation  
29 15 37.40  
Times: CPU Total Elapsed  
00:00:00.00 00:00:00.00  
Number of residues: 2036  
Number of sequences searched: 12  
Number of scores above cutoff: 12

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Stg.	Frame
1. A1978199_5	**** 2 standard deviations above mean ****	146	109	109	2.14	0
2. A1734448_4	**** 0 standard deviation from mean ****	194	109	109	2.14	0
3. A1734448_5		193	20	49	-0.24	0
4. A1978199_6	TOIG of: a1978199 check: 48	146	18	49	-0.29	0
5. A1978199_1	TOIG of: a1734448 check: 640	147	15	50	-0.37	0
6. A1734448_1		194	15	50	-0.37	0
7. A1734448_6		192	14	47	-0.40	0
8. A1978199_4		147	11	47	-0.48	0
9. A1978199_3		146	10	39	-0.51	0
10. A1978199_2		146	10	53	-0.51	0
11. A1734448_3		192	10	42	-0.51	0
12. A1734448_2		193	10	52	-0.51	0

1. SEQ-5\_2 (1-110)  
A1978199\_5  
Initial Score = 109  
Residue Identity = 99%  
Gaps = 0  
Optimized Score = 109  
Matches = 109  
Conservative Substitutions = 0  
Significance = 2.14  
Mismatch = 1

60 70 80 90 100 110 120 130 140  
X  
DNLVHPMKRGSTWALXGRDPRLLDSSMSNELCRLXACGKRRKXKXVNTROL  
HODCPSSRTSYVADNVLVHPMKRGSTWALXGRDPRLLDSSMSNELCRLXACGKRRKXKXVNTROL  
10 X 20 30 40 50 60 70  
AKKAVINNATLFFFWVHVAEKQONICFLILGITFPXGLEMAVYTLHERKS  
AKKAVINNATLFFFWVHVAEKQONICFLILGITFPXGLEMAVYTLHERKSARGQRMHLELFFCWIGOLT  
80 90 100 110 120 130 140  
CF

2. SEQ-5\_2 (1-110)  
A1734448\_4  
Initial Score = 109  
Residue Identity = 98%  
Gaps = 0  
Optimized Score = 109  
Matches = 108  
Conservative Substitutions = 0  
Significance = 2.14  
Mismatch = 2

50 60 70 80 90 100 110 120 130 140  
X  
DNLVHPMKRGSTWALXGRDPRLLDSSMSNELCRLXACG  
VARTGNSDPSLXRDXXDDACPSRPTSYVADNVLVHPMKRGSPWALXGRDPRLLDSSMSNELCRLXACG  
10 20 30 X 40 50 60 70  
EGNDKRXKXKXVNTROLAKKAVINNATLFFFWVHVAEKQONICFLILGITFPXGLEMAVYTLHERKS  
EGNDKRXKXKXVNTROLAKKAVINNATLFFFWVHVAEKQONICFLILGITFPXGLEMAVYTLHERKSAR  
80 90 100 110 120 130 140 X  
GQRHMLELFFPCWIGOLPCFVIRXSIAPLVKPDVNLXKKKKKKKKK  
150 160 170 180 190

3. SEQ-5\_2 (1-110)  
A1734448\_5  
Initial Score = 20  
Residue Identity = 12%  
Gaps = 0  
Optimized Score = 49  
Matches = 14  
Conservative Substitutions = 4  
Significance = -0.24  
Mismatch = 92

```

X 10 20 30 40
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQ
SGGLAIVTPPFDVPMKXRMMPAPPGPVSMQMLLSTLGNEGPLGFKAI PRFWIAPLCA MNPAGYELAK
10 20 30 X 40 50 60 70
EGNDKREKQXVNTDRLAKKAVINHA TFLFYFWVHVAEKOONICLFLIGITFPXGLEMAVXYTLHKS
50 60 70 80 90 100 110
KAMIKDEKNSSESTREILPRKQXSTMQLFYIFGSMLOQRNRTSAFPXYWELHSRALRMLYSIHYMKVLE
80 90 100 110 120 130 140 X
DRGCMSCSCFAGXDSLVLLSADDPKPSILNPMXICSKKKKKKKK
150 160 170 180 190

4. SEQ-5_2 (1-110)
AI978199_6
Initial Score ~ 18 Optimized Score ~ 49 Significance ~ -0.29
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 92
Gaps ~ 0 Conservative Substitutions ~ 4

X 10 20 30 40 50
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQEGNDKREKQXVNTDRL
TRTAPRPTPYSMQMLLSTLGNEGPLGFKAI PRFWIAPLCA MNPAGYELAKKAMIKDEKNSSESTREIL
10 X 20 30 40 50 60 70
60 70 80 90 100 110
AKKAVINHA TFLFYFWVHVAEKOONICLFLIGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70
PRKQXSTMQLFYIFGSMLOQRNRTSAFPXYWELHSRALRMLYSIHYMKVLEDRGCMSCSCFAGXDSLV
80 90 100 110 120 X 130 140

VL

5. SEQ-5_2 (1-110)
AI978199_1 TOIG of: a1978199 check: 48 from: 1 to: 442
Initial Score ~ 15 Optimized Score ~ 50 Significance ~ -0.37
Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 93
Gaps ~ 0 Conservative Substitutions ~ 5

X 10 20 30 40 50 60 70
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQEGNDKREKQXVNTDRLAKKAVINHA TFL
NKTSELSYPAKKEQQLQHVPLSSSTFLMXCILYSHLAKALRECNQYOKKADVULLLCMDPKIKKXSCMDVHC
X 10 20 30 40 50 60 70
FYFWVHVAEKOONICLFLIGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70
FLGKISRVDLEFFSSFIILAFKSSYPAKFIAPRGAIQKRGIAPLKSPSPPRMDKIIICIDTGVPGGA
80 90 100 110 X 120 130 140

VLV

6. SEQ-5_2 (1-110)
AI734448_1 TOIG of: a1734448 check: 6406 from: 1 to: 582
Initial Score ~ 15 Optimized Score ~ 50 Significance ~ -0.37
Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 93
Gaps ~ 0 Conservative Substitutions ~ 5

X 10 20 30 40
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQ
FEFFFEFFFEFLQIYIGFNKEGYSSADNKTRELSTYPAKEQQLQHVPLSSSTFLMXCILYSHLAKALRECN

```

```

10 20 30 X 40 50 60 70
GNDKREKQXVNTDRLAKKAVINHA TFLFYFWVHVAEKOONICLFLIGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70
QYOKKADVULLLCMDPKIKKXSCMDVHCFLGKISRVDLEFFSSFIILAFKSSYPAKFIAPRGAIQKRGCI
80 90 100 110 120 130 140
APLKSPPRMDKIIICIDTGVPGGAGIILAFITSKGCVTIAS
150 160 170 180 190

7. SEQ-5_2 (1-110)
AI734448_6
Initial Score ~ 14 Optimized Score ~ 47 Significance ~ -0.40
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 89
Gaps ~ 0 Conservative Substitutions ~ 7

X 10 20 30 40
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQ
LEDLRQXXPLPLTFXXLXGCLPLQAHQCLCRXXSCPSELTFRVPLGSLRARSPPASSGILLLEOXTLQAMSLPR
10 20 30 X 40 50 60 70
EGNLYKREKQXVNTDRLAKKAVINHA TFLFYFWVHVAEKOONICLFLIGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70
RQXXKMRKIPVSOHERSCQSDOPCNFFILFLGPPCCREATENHLPFPDIGNYIPVGPXDCIYVITYTEKCR
80 90 100 110 120 130 140 X
TEAHAGAVULLDRTAPLFCYPPRIHSLPCXTRCKEFLAKKKKKKKK
150 160 170 180 190

3. SEQ-5_2 (1-110)
AI978199_4
Initial Score ~ 11 Optimized Score ~ 47 Significance ~ -0.48
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 89
Gaps ~ 0 Conservative Substitutions ~ 7

X 10 20 30 40 50
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQEGNDKREKQXVNTDRL
APG..PLQAHQCLCRXXSCPSELTFRVPLGSLRARSPPASSGILLLEOXTLQAMSLPRRQXXMRKIPVSOHERS
10 X 20 30 40 50 60 70
LAKKAVINHA TFLFYFWVHVAEKOONICLFLIGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70
COHSSDOPCNFFILFLGPPCCREATENHLPFPDIGNYIPVGPXDCIYVITYTEKCRTEAHAGAVULLDRTAH
80 90 100 110 120 X 130 140

LFC

9. SEQ-5_2 (1-110)
AI978199_3
Initial Score ~ 10 Optimized Score ~ 39 Significance ~ -0.51
Residue Identity ~ 11% Matches ~ 11 Mismatches ~ 85
Gaps ~ 0 Conservative Substitutions ~ 2

X 10 20
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQEGNDKREKQXVNTDRLAKKAVINHA TFLFYFWVHVAEKOONICLFLIGITFPX
10 20 30 40 50 60 70 80 90
QNK<AVI>SKRTTAPACASVLXHFSHVMTIOPSOCPGKXPPISKGRCSVASIQHGPKNKIKKLHGXSLL
10 20 30 40 50 60 70
DCCSSWSNELCRLXACQEGNDKREKQXVNTDRLAKKAVINHA TFLFYFWVHVAEKOONICLFLIGITFPX

```





This Page Blank (uspto)

Init. Opt.

Sequence Name	Description	Length	Score	Score	Sig.	Frame
1. A1978199	<i>translational frame</i>	147	111	111	2.16	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
---------------	-------------	--------	-------------	------------	------	-------

2.	AI734448_6	****	0	standard deviation	from mean	****	192	110	110	2.13	0
3.	AI978199_3						146	15	48	-0.37	0
4.	AI734448_3						192	15	48	-0.37	0
5.	AI978199_2						146	14	43	-0.40	0
6.	AI734448_5						193	14	33	-0.40	0
7.	AI734448_2						193	14	48	-0.40	0
8.	AI978199_6						146	13	17	-0.42	0
9.	AI978199_5						146	13	49	-0.42	0
10.	AI978199_1	TOIG of:	ai978199	check:	48		147	12	50	-0.45	0
11.	AI734448_1	TOIG of:	ai734448	check:	640		194	12	50	-0.45	0
12.	AI734448_4						194	9	49	-0.53	0

```

1. SEQ-5_1 (1-111)
   A1578199_4
Initial Score = 111 Optimized score = 111 Significance = 2.16
Residue Identity = 100% Matches = 111 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

[illegible]

0.57

```

2. SEQ5_1 (1-111)
   A1731448_6
Initial Score = 110 Optimized Score = 110 Significance = 2.13
Residue Identity = 99% Matches = 110 Mismatches = 1
Caps 0 Conservative Substitutions 0

```

[illegible]3. SEQ-5-1 (1-111)  
AT978199\_3





This Page Blank (uspto)

> O <  
O I O < Intelligence  
> O <

FastD - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file seq-5\_3.res made by bobryen on Thu 28 Feb 102 15:45:52-PSW.

Query sequence being compared: SEQ-5\_3 (1-109)  
Number of sequences searched: 12  
Number of scores above cutoff: 12

Results of the initial comparison of SEQ-5\_3 (1-109) with:  
File: genbanktrans.pep

*Seq 5, translation frame 3*

```

100-
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
E -
U -
Q -
E -
N -
C -
S -
SCORE 0 121 24 36 481 60 72 841 96 108
STDEV 0 1 1 1 1 1 1 1 1 1

```

# PARAMETERS

Similarity matrix PAM-150 K-tuple 1  
Threshold level of sim. 16%  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 5.00 Window size 109  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean 31 Median 19 Standard Deviation 35.91  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 2036  
Number of sequences searched: 12  
Number of scores above cutoff: 12

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sign.	Frame
1. A1978199_6	**** 2 standard deviations above mean ****	146	108	108	2.14	0
2. A1734448_5	**** 0 standard deviation from mean ****	193	108	108	2.14	0
3. A1734448_6		192	22	49	-0.25	0
4. A1978199_4		147	21	48	-0.28	0
5. A1978199_5		146	19	47	-0.33	0
6. A1734448_4		194	19	48	-0.33	0
7. A1978199_1		147	18	37	-0.36	0
8. A1734448_1	TOIG of: a1978199 check: 48	194	18	44	-0.36	0
9. A1978199_2	TOIG of: a1734448 check: 640	146	13	49	-0.50	0
10. A1978199_3		146	13	49	-0.50	0
11. A1734448_3		192	11	52	-0.56	0
12. A1734448_2		193	11	49	-0.56	0

1. SEQ-5\_3 (1-109)  
A1978199\_6  
Initial Score = 108 Optimized Score = 108 Significance = 2.14  
Residue Identity = 99% Matches = 108 Mismatches = 1  
Gaps = 0 Conservative Substitutions = 0

```

X 10 20 30 40 50
TTLSTLGNBGLGKGAIPGFVIAPIGLAMNFAGYELAKKAMIKDEKNSSESTREIL
PRKXSTNMLFFYFIFGSMLOQSNRTSAFFXYWELHSRRALRWLYSIHYMRK
PRKXSTNMLFFYFIFGSMLOQSNRTSAFFXYWELHSRRALRWLYSIHYMRK
PRKXSTNMLFFYFIFGSMLOQSNRTSAFFXYWELHSRRALRWLYSIHYMRK
80 90 100 110 120 130 140
VL

```

2. SEQ-5\_3 (1-109)  
A1734448\_5  
Initial Score = 108 Optimized Score = 108 Significance = 2.14  
Residue Identity = 99% Matches = 108 Mismatches = 1  
Gaps = 0 Conservative Substitutions = 0

```

X 10 20 30 40
SGLLAIVTPPPDVMKXRMPPAPCPBPVSMOMITLISLGNBGLGKGAIPGFVIAPIGLAMNFAGYELAK
KAMIDKNSSESTREILPRKXSTNMLFFYFIFGSMLOQSNRTSAFFXYWELHSRRALRWLYSIHYMRK
KAMIDKNSSESTREILPRKXSTNMLFFYFIFGSMLOQSNRTSAFFXYWELHSRRALRWLYSIHYMRK
80 90 100 110 120 130 140
CGTCGSCCFAAGXDSLVLSADDPXPSSLNPMXICSKKKKKKK
150 160 170 180 190

```

3. SEQ-5\_3 (1-109)  
A1734448\_6  
Initial Score = 22 Optimized Score = 49 Significance = -0.25  
Residue Identity = 108 Matches = 16 Mismatches = 83  
Gaps = 44 Conservative Substitutions = 10

```

X 10 20 30 40
IILSLGNEGPLGFKGAIPEFWIAPLGAMNFAGYELAK
LEDLROXXPLPLTXXLXCLPLQAOHOCICRXXSCPSLETFRVPLGSLRARSBPASSGLLLEQXOXTLQAMSLPR
10 20 30 X 40 50 60 70
KAMIKDEKNSSESTREILPRKQXSTWOLFTEIF-----
50 60 70
ROXXKKMRKIVSOHERSCOESSDQPCNFEFLILGPPCCREATEHLLPFEDIGNVYIPVGXDCIYITTEKCYR
80 90 100 110 120 130 140
-----GSMLOQRNRTSAFXYWELHSRRALRWLYSIHYMRK
150 160 170 180 X 190
TEAHGAVVLLDRTAPLFCYPRMHSLPCTRCCKFALKKKKKKKK

4. SEQ-5_3 (1-109)
AI978199_4
Initial Score = 21 Optimized Score = 48 Significance = -0.28
Residue Identity = 11% Matches = 13 Mismatches = 89
Gaps = 0 Conservative Substitutions = 7

X 10 20 30 40 50
IILSLGNEGPLGFKGAIPEFWIAPLGAMNFAGYELAKKAMIKDEKNSSESTREI
APGILPLQAOHOCICRXXSCPSLETFRVHLSLARSPASSGLLLEQXOXTLQAMSLPRROXXKKMRKIPVSOHERS
10 X 20 30 40 50 60 70
50 70 80 90 100 X
LPRKQXSTWOLFTEIFGSMLOQRNRTSAFXYWELHSRRALRWLYSIHYMRK
COESSDQPCNFEFLILGPPCCREATEHLLPFEDIGNVYIPVGXDCIYITTEKCYRTEAHGAVVLLDRTAH
80 90 100 110 120 X 130 140
LFC

5. SEQ-5_3 (1-109)
AI978199_5
Initial Score = 19 Optimized Score = 47 Significance = -0.33
Residue Identity = 6% Matches = 7 Mismatches = 93
Gaps = 0 Conservative Substitutions = 9

X 10 20 30 40 50
IILSLGNEGPLGFKGAIPEFWIAPLGAMNFAGYELAKKAMIKDEKNSSESTREI
HODCPNHTSVYADDNLVHPMKRGSTWALGRDPLLDCCSWSNLCRLXACQEGDKRKEKFOXYNTBTL
10 X 20 30 40 50 60 70
60 70 80 90 100 X
LPRKQXSTWOLFTEIFGSMLOQRNRTSAFXYWELHSRRALRWLYSIHYMRK
AKKAVINHAATFLEFWVHVAEKOQNICLFILGITFPXGLEMAVXYTLHESARGORHMLLEFFCWIGULT
80 90 100 110 120 X 130 140
CP

6. SEQ-5_3 (1-109)
AI734448_4
Initial Score = 19 Optimized Score = 48 Significance = -0.33
Residue Identity = 7% Matches = 8 Mismatches = 92
Gaps = 0 Conservative Substitutions = 9

X 10 20 30

```

```

IILSLGNEGPLGFKGAIPEFWIAPLGAMNFAGYELAK
VWRYCGNSDPSLXREDDXDAICPSRPTSVYADDNLVHPMKRGSPWALXGRDPLLDCCSWSNLCRLXACQ
10 20 30 X 40 50 60 70
KAMIKDEKNSSESTREILPRKQXSTWOLFTEIFGSMLOQRNRTSAFXYWELHSRRALRWLYSIHYMRK
40 50 60 70 80 90 100 X
EGNDRKREKFOXYNTBTLDAKKAVINHAATFLEFWVHVAEKOQNICLFILGITFPXGLEMAVXYTLHESARG
80 90 100 110 120 130 140 X
GQRHMLLEFFCWIGULTPCFYIRKXSIAFLVKKPDVNLKKKKKKKK
150 160 170 180 190

7. SEQ-5_3 (1-109)
AI978199_1 TOIG of: AI978199 check: 48 from: 1 to: 442
Initial Score = 18 Optimized Score = 37 Significance = -0.36
Residue Identity = 4% Matches = 4 Mismatches = 75
Gaps = 0 Conservative Substitutions = 5

X 10 20
IILSLGNEGPLGFKGAIPEF
OLOHVPSSSTFLMXCILYSHLALRECNQYOKKADVYLLLCNMDPKIKKSCWVDHCFLGKISRVDSEF
20 30 40 50 60 X 70 80
FWIAPLGAMNFAGYELAKKAMIKDEKNSSESTREILPRKQXSTWOLFTEIFGSMLOQRNRTSAFXYWELHS
100 110 120 130 140 X
FSSVITAFIASSXPAKFIAPRGATOKKRGIAPLKSPSPSPRPMDKIIICIDTGPVGCALV
90 100 110 120 130 140 X
RFZRWLYSIHYMRK

8. SEQ-5_3 (1-109)
AI734448_1 TOIG of: AI734448 check: 6406 from: 1 to: 582
Initial Score = 18 Optimized Score = 44 Significance = -0.36
Residue Identity = 11% Matches = 11 Mismatches = 77
Gaps = 0 Conservative Substitutions = 6

X 10 20
IILSLGNEGPLGFKGAIPEF
SSTFLMXCILYSHLALRECNQYOKKADVYLLLCNMDPKIKKSCWVDHCFLGKISRVDSEFFSFI
60 70 80 90 100 110 120
FWIAPLGAMNFAGYELAKKAMIKDEKNSSESTREILPRKQXSTWOLFTEIFGSMLOQRNRTSAFXYWELHS
100 110 120 130 140 150 160 170 180 190 X
LASSXPAKFIAPRGATOKKRGIAPLKSPSPSPRPMDKIIICIDTGPVGCALVILKFTSGVTTIASPD
130 140 150 160 170 180 190 X
FKALRWLYSIHYMRK

9. SEQ-5_3 (1-109)
AI978199_2
Initial Score = 13 Optimized Score = 49 Significance = -0.50
Residue Identity = 10% Matches = 11 Mismatches = 87
Gaps = 0 Conservative Substitutions = 11

X 10 20 30 40 50
IILSLGNEGPLGFKGAIPEFWIAPLGAMNFAGYELAKKAMIKDEKNSSESTREI
TKQVSCPIQOKNNSSMCICPLALFSCNVYTTALSRPYGVNIPIMIKRQMPCCSATWTQXKKKXVAMLTA
10 X 20 30 40 50 60 70

```



60 70 80 90 100  
 ILPRKXSTWOLFYIFGSMLORSNRTSAFFYWEHLSRRALWLSIHYMRK X  
 FLARSLVLTWNNFSLSLPSWQAHSLQSLQEQSRSGSRPRRAQVDPFRQGWTRLSAXTLVLCLEGO  
 80 90 100 110 120 130 140

SW

10. SEQ-5\_3 (1-109)  
 AT978199\_3

Initial Score = 11 Optimized Score = 52 Significance = -0.56  
 Residue Identity = 15% Matches = 17 Mismatches = 86  
 Gaps = 0 Conservative Substitutions = 6

60 70 80 90 100 110 120 130 140 150 160 170  
 QNKXAVLSKRTTAPACASVLAHFHSHVYTIOPSGPTGMKFPISKGRCSVASLQHGPKNKIKKLGXSL  
 10 20 30 40 50 60 70

60 70 80 90 100 110 120 130 140 150 160 170  
 TREILPRKXSTWOLFYIFGSMLORSNRTSAFFYWEHLSRRALWLSIHYMRK X  
 SWQDLSXCLTGTIFLFYHCLLGKLTACVHCSCRSNPEAGDRALKEPKWTLYSKDGDYHLHRHWCAMRGS  
 80 90 100 110 120 130 140 150 160 170

PG

11. SEQ-5\_3 (1-109)  
 AT734448\_3

Initial Score = 11 Optimized Score = 52 Significance = -0.56  
 Residue Identity = 15% Matches = 17 Mismatches = 86  
 Gaps = 0 Conservative Substitutions = 6

60 70 80 90 100 110 120 130 140 150 160 170  
 FFFRFFFRANLHRYXOGRMTWIGGXONKGAVALSSKRTTAPACASVLAHFHSHVYTIOPSGPTGMKFP  
 10 20 30 40 50 60 70

60 70 80 90 100 110 120 130 140 150 160 170  
 IAPLGAMNFAGYELAKKAMIKDEKNSSESTREILPRKXSTWOLFYIFGSMLORSNRTSAFFYWEHLSRR  
 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170  
 ISKGRCSVASLQHGPKNKIKKLGXSLQSLQEQSRSGSRPRRAQVDPFRQGWTRLSAXTLVLCLEGO  
 80 90 100 110 120 130 140 150 160 170

100 X  
 ALRWLSIHYMRK  
 11:  
 ALKEPKGTLVSKDGDYHLHRHWMAMRGHHPXLHRYVKGCHYCKRSS  
 150 160 170 180 190

12. SEQ-5\_3 (1-109)  
 AT734448\_2

Initial Score = 11 Optimized Score = 49 Significance = -0.56  
 Residue Identity = 10% Matches = 11 Mismatches = 87  
 Gaps = 0 Conservative Substitutions = 11

60 70 80 90 100 110 120 130 140 150 160 170  
 FFFRFFFRXSKFTSGLTRKAMDHRITTKGSCPIQKNNSSMCLCPALFLFCNVYVYTAISRXYGVIP  
 10 20 30 40 50 60 70

30 40 50 60 70 80 90 100 110 120 130 140  
 LGAMNFAGYELAKKAMIKDEKNSSESTREILPRKXSTWOLFYIFGSMLORSNRTSAFFYWEHLSRRAL  
 NIKKQMECCFSATWTQXKKNKVAAMLITAFLARSLVLTWNNFSLSLPSWQAHSLQSLQEQSRSGGS  
 80 90 100 110 120 130 140  
 WLSIHYMRK X  
 100 X  
 RPYRAQGDPRFQGWTRLSAXTLVLCLEGOASSXSSROREGSLLPOVLO  
 150 X 160 170 180 190

This Page Blank (uspto)

; Entered [bobyen 28-Feb-02 15:41]

SEQ-5\_1  
XXCPSLEFTRVHIGSLRARSPASSGILLLEOXTLQAMSLPRROXXKKRKIPVSOHERSCQESSDOPCNFF  
ILFLGPCREATEHLPPFDIGNYIPVGPYDGCIVITYXECI

SEQ-5\_2  
DNLVHFMKRGSTWALXGRDPRLLDCSSNSNEICRLXACOEGNDKRXEKFQXVNTDOLAKKAVINHATEL  
FYFWHVAERQONICLFLILGITFPYGLEMAVYVTLHEKSI

SEQ-5\_3  
ILSTIGNEGPLGLFRGAIIPGFPIAPLGAMNFAGYELAKKAMI KDEKNSESTREILPRKXSTWOLFV  
FITGSMLOQSNRTSAFFPYWELHSRRLRWLYSIHYMRKI

SEQ-5\_4  
ALFSCNVYVTAISRPGNVIPNKKROMFCCFSATWOKXKKVAVMLITAFARSLVLTWMPSHLSLP  
SMOAHSLQSSLLQEOSSRRSGSRPXRAQVDPFRQGWTRLISL

SEQ-5\_5  
HESHVMTTTPSGOPTGMAMPISKKRCVASYLQHGPKNKIKKLHGXSLSMODLSCXLTGIFLIFYHCL  
LGLLACKVHCSCRSNPEEGDRALKEPKWTLVSKDGDYI

SEQ-5\_6  
TFLMXCILYSHLALRECNQYOKKADVLLLLCNMDPKIKXKSCWVDHCFLGKISRVDSEFFSFIIAF  
LASSYPAKFIAPRGAIQKKGINPLKSPSGPSFPRMDKI

**This Page Blank (uspto)**

**RESULTS:** 1  
**LOCUS:** AI978199/c  
**DEFINITION:** 614041D10.x2 614 - root cDNA library from Walbot Lab: Zea mays cDNA, mRNA sequence.  
**ACCESSION:** AI978199  
**VERSION:** AI978199.1 GI:5791407  
**KEYWORDS:** EST.  
**SOURCE:** Zea mays.  
**ORGANISM:** Zea mays  
**EC:** Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae  
**CAZ:** Andropogoneae; Zea.  
**REFERENCE:** 1 (bases 1 to 442)  
**AUTHORS:** Walbot, V.  
**TITLE:** Maize ESTs from various cDNA libraries sequenced at Stanford University  
**JOURNAL:** Unpublished (1999)  
**COMMENT:** Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 614041 row: D column: 10.  
**FEATURES:**  
 source  
 Location/Qualifiers  
 1..442  
 /organism="Zea mays"  
 /cultivar="W23"  
 /db\_xref="taxon:4577"  
 /clone\_lib="614 - root cDNA library from Walbot Lab"  
 /tissue\_type="root"  
 /dev\_stage="3-4 days old"  
 /lab\_host="XL0LR"  
 /note="Organ: root; Vector: pBlueScriptII SK+; Site\_1: EcoRI; Site\_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"  
**BASE COUNT:** 126 a 107 c 93 g 116 t  
**ORIGIN:**

Query Match 99.5%; Score 331.4; DB 104; Length 442;  
 Best Local Similarity 99.7%; Pred. No. 5e-85;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	tgataatcttgtccatccttggaaacgaggggtccacttgggctctttaagggcgcgatcc	60
Db	400	TGATAATCTTGTCCATCCTTGGAAACGAGGGTCCACTTGGGCTCTTTAAGGGCGCGATCC	341
QY	61	ccgcttcttcttgattgctcctcttggagcaatgaactttgcaggctatgagcttgcca	120
Db	340	CCGCTTCTTCTTGATTGCTCCTCTTGGAGCAATGAACCTTGCAGGCTATGAGCTTGCCA	281
QY	121	agaaggcaatgataaaagatgagaaaaattccagtgagtcaacacgagagatcttgccaa	180
Db	280	AGAAGGCAATGATAAAAGATGAGAAAAATCCAGTGAGTCAACACGAGAGATCTTGCCAA	221
QY	181	gaaagcagtgatcaaccatgcaactttttttattttttgggtccatgttgagagaa	240
Db	220	GAAAGCAGTGATCAACCATGCAACTTTTTTATTTTATTTTGGGTCCATGTTGAGAGAA	161
QY	241	gcaacagaaacatctgccttttttgatattgggaattacattcccgtagggccttgagat	300
Db	160	GCAACAGAACATCTGCCTTTTTTGATATTGGGAATTACATCCCGTAGGGCCTTGAGAT	101
QY	301	ggctgtatagtatacattacatgagaaaagtgc	333
Db	100	GGCTGTATAGTATACATTACATGAGAAAAGTGC	68

**This Page Blank (uspto)**

Alanine	ala	A	G C N
cysteine	cys	C	U G U U G C
Aspartic Acid	Asp	D	G A U G A C
Glutamic acid	Glu	E	G A A G A G
Phenylalanine	phe	F	U U U U U C
Glycine	gly	G	G G N
Histidine	his	H	C A U C A C
isoleucine	Ile	I	A A U A U C A U A
Lysine	lys	K	A A A A A G
leucine	leu	L	U U U U U G C U N
Methionine	met	M	A U G
Asparagine	asn	N	A A U A A C
Proline	pro	P	C C N
Glutamine	gln	Q	C C A C A G
Arginine	arg	R	C G N A G A A G G
serine	ser	S	U C N A G U A G C
Threonine	thr	T	C A N
valine	val	V	G U N
Tryptophan	trp	W	U G G
Tyrosine	tyr	Y	U A U U A C
STOP			U A A U A G U G A
START			A U G

This Page Blank (uspto)





**This Page Blank (uspto)**